

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/569,766  
Source: JFWP  
Date Processed by STIC: 03/06/2006

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/569,766</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor <b>after</b> creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. <b>Do not use tab codes between numbers; use space characters</b> , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was <b>not</b> saved in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only <b>valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input checked="" type="checkbox"/> Use of <220>	<del>Sequence(s) <input type="checkbox"/> missing the &lt;220&gt; "Feature" and associated numeric identifiers and responses. Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if &lt;213&gt; "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in &lt;220&gt; to &lt;223&gt; section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules.</del>	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can <b>only</b> represent a single <u>nucleotide</u> ; "Xaa" can <b>only</b> represent a single <u>amino acid</u>	



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/569,766

DATE: 03/06/2006  
TIME: 13:35:24

Input Set : A:\GENOM.032NP.TXT  
Output Set: N:\CRF4\03062006\J569766.raw

4 <110> APPLICANT: Crothers, Donald M.  
6 <120> TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUESTERING AGENTS AND  
7 METHODS OF USE  
9 <130> FILE REFERENCE: GENOM.032NP  
-> 11 <140> CURRENT APPLICATION NUMBER: US/10/569,766  
-> 11 <141> CURRENT FILING DATE: 2006-02-23  
11 <150> PRIOR APPLICATION NUMBER: PCT/US2004/027412  
12 <151> PRIOR FILING DATE: 2004-08-23  
14 <150> PRIOR APPLICATION NUMBER: 60/497,821  
15 <151> PRIOR FILING DATE: 2003-08-25  
17 <160> NUMBER OF SEQ ID NOS: 26  
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 54  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Homo sapiens  
26 <400> SEQUENCE: 1  
27 tctgttaagag cagatccctg gacaggcaag gaatacagag ggcagcagac atcg  
29 <210> SEQ ID NO: 2  
30 <211> LENGTH: 27  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Artificial Sequence  
34 <220> FEATURE:  
35 <223> OTHER INFORMATION: First complementary nucleic acid  
37 <400> SEQUENCE: 2  
38 gcctgtccag ggtatctgctc ttacaga  
40 <210> SEQ ID NO: 3  
41 <211> LENGTH: 22  
42 <212> TYPE: DNA  
43 <213> ORGANISM: Artificial Sequence  
45 <220> FEATURE:  
46 <223> OTHER INFORMATION: Second complementary nucleic acid  
48 <400> SEQUENCE: 3  
49 ggacaaaaata cctgtattcc tt  
51 <210> SEQ ID NO: 4  
52 <211> LENGTH: 41  
53 <212> TYPE: DNA  
54 <213> ORGANISM: Artificial Sequence  
56 <220> FEATURE:  
57 <223> OTHER INFORMATION: n=dideoxyG  
59 <220> FEATURE:  
60 <223> OTHER INFORMATION: Sequestering agent  
62 <400> SEQUENCE: 4

CPG-6)  
Does Not Comply  
Corrected Diskette Needed

(CPG 1, 2, 3, 4, 5)

54

27

Invalid Response. What is the  
Source of genetic  
Material. P/S see  
Item 11 on Error  
Summary  
Sheet

22

OK

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/569,766

DATE: 03/06/2006

TIME: 13:35:24

Input Set : A:\GENOM.032NP.TXT  
 Output Set: N:\CRF4\03062006\J569766.raw

```

-> 63 gatccctgga caggccggaa gcggctttt tgccgcttcc n          41
 65 <210> SEQ ID NO: 5
 66 <211> LENGTH: 41
 67 <212> TYPE: DNA
 68 <213> ORGANISM: Artificial Sequence
 70 <220> FEATURE:
 71 <223> OTHER INFORMATION: Sequestering agent
 73 <400> SEQUENCE: 5
 74 gtgccgagac gtttttcgt ctcggacta ggaatacagg t          41
 76 <210> SEQ ID NO: 6
 77 <211> LENGTH: 26
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial Sequence
 81 <220> FEATURE:
 82 <223> OTHER INFORMATION: First complementary nucleic acid
 84 <400> SEQUENCE: 6
 85 ctccccgaga caccttctcc ttcaag                          26
 87 <210> SEQ ID NO: 7
 88 <211> LENGTH: 15
 89 <212> TYPE: DNA
 90 <213> ORGANISM: Artificial Sequence
 92 <220> FEATURE:
 93 <223> OTHER INFORMATION: Second complementary nucleic acid
 95 <400> SEQUENCE: 7
 96 ttagatgatgaa atcgg                                     15
 98 <210> SEQ ID NO: 8
 99 <211> LENGTH: 15
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Third complementary nucleic acid
106 <400> SEQUENCE: 8
107 ttagatgatgaa atcga                                     15
109 <210> SEQ ID NO: 9
110 <211> LENGTH: 39
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: n=dideoxyG
117 <220> FEATURE:
118 <223> OTHER INFORMATION: First sequestering agent
120 <400> SEQUENCE: 9
-> 121 ggtgtctgcg ggagcggaaag cggcttttg ccgcttccn          39
123 <210> SEQ ID NO: 10
124 <211> LENGTH: 37
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Second sequestering agent

```

Some end  
Some end

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/569,766

DATE: 03/06/2006

TIME: 13:35:24

Input Set : A:\GENOM.032NP.TXT

Output Set: N:\CRF4\03062006\J569766.raw

131 <400> SEQUENCE: 10  
 132 gctgcaccgc tttttgcgg tgcacccgat ttcatca 37  
 134 <210> SEQ ID NO: 11  
 135 <211> LENGTH: 37  
 136 <212> TYPE: DNA  
 137 <213> ORGANISM: Artificial Sequence  
 139 <220> FEATURE:  
 140 <223> OTHER INFORMATION: Third sequestering agent  
 142 <400> SEQUENCE: 11  
 143 gctgcaccgc tttttgcgg tgcactcgat ttcatca 37  
 145 <210> SEQ ID NO: 12  
 146 <211> LENGTH: 96  
 147 <212> TYPE: DNA  
 148 <213> ORGANISM: Artificial Sequence  
 150 <220> FEATURE:  
 151 <223> OTHER INFORMATION: RC probe  
 153 <400> SEQUENCE: 12  
 154 gcacccaaa gctgttccgt cccagttgac tattcctcgtt gaattcttagc tactggcaat 60  
 155 ctgatcccta tagtgagtcg tattacaggc acaaac 96  
 157 <210> SEQ ID NO: 13  
 158 <211> LENGTH: 15  
 159 <212> TYPE: DNA  
 160 <213> ORGANISM: Artificial Sequence  
 162 <220> FEATURE:  
 163 <223> OTHER INFORMATION: Z tag  
 165 <400> SEQUENCE: 13  
 166 agctactggc aatct 15  
 168 <210> SEQ ID NO: 14  
 169 <211> LENGTH: 20  
 170 <212> TYPE: DNA  
 171 <213> ORGANISM: Artificial Sequence  
 173 <220> FEATURE:  
 174 <223> OTHER INFORMATION: T7 promoter  
 176 <400> SEQUENCE: 14  
 177 ccctatacgatg agtcgttatta 20  
 179 <210> SEQ ID NO: 15  
 180 <211> LENGTH: 6  
 181 <212> TYPE: DNA  
 182 <213> ORGANISM: Artificial Sequence  
 184 <220> FEATURE:  
 185 <223> OTHER INFORMATION: Eco RI site  
 187 <400> SEQUENCE: 15  
 188 gaattc  
 190 <210> SEQ ID NO: 16  
 191 <211> LENGTH: 3  
 192 <212> TYPE: DNA  
 193 <213> ORGANISM: Artificial Sequence  
 195 <220> FEATURE:  
 196 <223> OTHER INFORMATION: 3' nucleotide gap

gene  
gene  
joined

## RAW SEQUENCE LISTING

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Input Set : A:\GENOM.032NP.TXT  
 Output Set: N:\CRF4\03062006\J569766.raw

198 <400> SEQUENCE: 16  
 199 gat 3  
 201 <210> SEQ ID NO: 17  
 202 <211> LENGTH: 13  
 203 <212> TYPE: DNA  
 204 <213> ORGANISM: Artificial Sequence  
 206 <220> FEATURE:  
 207 <223> OTHER INFORMATION: Sequence complementary to p53  
 209 <400> SEQUENCE: 17 13  
 210 caggcacaaa cac  
 212 <210> SEQ ID NO: 18  
 213 <211> LENGTH: 24  
 214 <212> TYPE: DNA  
 215 <213> ORGANISM: Artificial Sequence  
 217 <220> FEATURE:  
 218 <223> OTHER INFORMATION: Sequence complementary to p53  
 220 <400> SEQUENCE: 18 24  
 221 gcacacctaaa gctgttccgt cccca  
 223 <210> SEQ ID NO: 19  
 224 <211> LENGTH: 21  
 225 <212> TYPE: DNA  
 226 <213> ORGANISM: Artificial Sequence  
 228 <220> FEATURE:  
 229 <223> OTHER INFORMATION: RC primer  
 231 <400> SEQUENCE: 19  
 232 gataggagtc acttaagatc g 21  
 234 <210> SEQ ID NO: 20  
 235 <211> LENGTH: 34  
 236 <212> TYPE: DNA  
 237 <213> ORGANISM: Homo sapiens  
 239 <400> SEQUENCE: 20  
 240 ctaatctgtta agagcagatc cctggacagg caag 34  
 242 <210> SEQ ID NO: 21  
 243 <211> LENGTH: 22  
 244 <212> TYPE: DNA  
 245 <213> ORGANISM: Homo sapiens  
 247 <400> SEQUENCE: 21  
 248 aaggaataaca ggtattttgt cc 22  
 250 <210> SEQ ID NO: 22  
 251 <211> LENGTH: 14  
 252 <212> TYPE: DNA  
 253 <213> ORGANISM: Artificial Sequence  
 255 <220> FEATURE:  
 256 <223> OTHER INFORMATION: F5 1698 T7 Probe  
 258 <400> SEQUENCE: 22  
 259 gcctgtccag ggat 14  
 261 <210> SEQ ID NO: 23  
 262 <211> LENGTH: 37  
 263 <212> TYPE: DNA

*some sort of*

RAW SEQUENCE LISTING  
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TIME: 13:35:24

Input Set : A:\GENOM.032NP.TXT  
Output Set: N:\CRF4\03062006\J569766.raw

264 <213> ORGANISM: Artificial Sequence  
266 <220> FEATURE:  
267 <223> OTHER INFORMATION: n=dideoxyG  
269 <220> FEATURE:  
270 <223> OTHER INFORMATION: Sequestering agent  
272 <400> SEQUENCE: 23  
-> 273 cctggacagg ccggaaagcggtttttgcc gcttccn 37  
275 <210> SEQ ID NO: 24  
276 <211> LENGTH: 25  
277 <212> TYPE: DNA  
278 <213> ORGANISM: Homo sapiens  
280 <400> SEQUENCE: 24  
281 aaggaataca ggtattttgt ctttg 25  
283 <210> SEQ ID NO: 25  
284 <211> LENGTH: 25  
285 <212> TYPE: DNA  
286 <213> ORGANISM: Artificial Sequence  
288 <220> FEATURE:  
289 <223> OTHER INFORMATION: Tag probe  
291 <400> SEQUENCE: 25  
292 caaggacaaa atacctgtat tcctt 25  
294 <210> SEQ ID NO: 26  
295 <211> LENGTH: 40  
296 <212> TYPE: DNA  
297 <213> ORGANISM: Artificial Sequence  
299 <220> FEATURE:  
300 <223> OTHER INFORMATION: Sequestering agent  
302 <400> SEQUENCE: 26  
303 gtgccgagac gtttttcgt ctcggcacaa ggaatacagg 40

-? Same error

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/06/2006  
PATENT APPLICATION: US/10/569,766 TIME: 13:35:25

Input Set : A:\GENOM.032NP.TXT  
Output Set: N:\CRF4\03062006\J569766.raw

**base Note:**

~~3 of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.~~

J#4; N Pos. 41

J#9; N Pos. 39

J#23; N Pos. 37

**VARIABLE LOCATION SUMMARY** DATE: 03/06/2006  
**PATENT APPLICATION:** US/10/569,766 **TIME:** 13:35:25

Input Set : A:\GENOM.032NP.TXT  
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### 3 of n's or Xaa's (NEW RULES):

~~None of n's and/or Xaa's have been detected in the Sequence Listing.~~

<sup>3</sup> of <220> to <223> is MANDATORY if n's or Xaa's are present.

<220> to <223> section, please explain location of n or Xaa, and which

side n or Xaa represents.

J#4; N Pos. 41

#9; N Pos. 39

#23; N Pos. 37

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/569,766

DATE: 03/06/2006

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Input Set : A:\GENOM.032NP.TXT

Output Set: N:\CRF4\03062006\J569766.raw

11 M:270 C: Current Application Number differs, Replaced Current Application No  
11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
53 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4  
53 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4  
53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
121 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9  
121 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9  
121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
273 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:23  
273 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:23  
273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0